

Amendments to the Specification

Please replace the paragraph appearing at page 5, lines 9-25 with the following amended paragraph:

Figure 2A-C show a physical map of the *P. syringae* pv. *tomato* DC3000 *hrpW* region, its conservation with a corresponding region in *P. syringae* pv. *syringae* B728a, and structural features of HrpW. Figure 2A shows a physical map of the DC3000 genome adjacent to the *hrp* gene cluster with open arrows denoting putative σ^{54} promoters and filled arrows denoting putative HrpL-dependent promoters that control previously defined transcriptional units (Lorang, J.M., et al., Mol. Plant-Microbe Interact., 8:49-57 (1995), which is hereby incorporated by reference). *hrpR* and *hrpS* encode regulatory proteins and are located at the right end of the *hrp* cluster. Numbers in boxes above the map give the percent identity of DC3000 DNA and colinearly arranged partial B728a DNA sequences. In Figure 2B, the diagram of HrpW indicates the hypersensitive response elicitor-like and pectate lyase ("Pel")-like domains. The PCR subclone-generated His₆-tagged hypersensitive response elicitor domain fragment encompasses amino acids 1-186; the His₆-tagged Pel domain has amino acids 187-425. Figure 2C shows the sequence of the region in the middle of HrpW that contains 6 glycine-rich repeats (see box) (aa 119-186 of SEQ ID NO: 2), with similar repeats in the HrpZ proteins from *P. syringae* pv. *tomato* ("Pto") (aa 121-128 = SEQ ID NO: 9, aa 234-244 = SEQ ID NO: 10, aa 285-295 = SEQ ID NO: 11), and *P. syringae* pv. *syringae* ("Pss") (aa 211-220 = SEQ ID NO: 12, aa 265-270 = SEQ ID NO: 13) aligned below. Dashes were introduced where necessary to preserve alignment.